

## SEQUENCE LISTING

&lt;110&gt; Applied Biosystems

5 Bolchakova, Elena V.

Rozzelle, James E.

&lt;120&gt; A Novel DNA Polymerase from the Thermophilic Thermus Scotoductus

10

&lt;130&gt; 1560.002W01

&lt;150&gt; US 60/334489

15&lt;151&gt; 2001-11-30

&lt;150&gt; US 60/322218

&lt;151&gt; 2000-09-14

20&lt;160&gt; 50

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

25&lt;211&gt; 2502

&lt;212&gt; DNA

&lt;213&gt; Thermus scotoductus

&lt;400&gt; 1

```

30atgagggcga tgctgccct ctttgagccc aagggccggg tgcttctggt ggacggccac      60
   cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg      120
   gtccaggcgg tgtacgggtt tgccaagagc cttttgaagg cgctaaggga agacggggat      180
   gtggtgatcg tgggtgttga cgccaaggcc ccctccttcc gccaccagac ctacgaggcc      240
   tacaaggcgg ggcgggctcc caccctcgag gactttcccc ggcagcttgc ccttatcaag      300
35gagatggtgg accttttggg cctggagcgc ctcgaggtgc cgggctttga ggcggatgac      360
   gtcctggcta ccctggccaa gaaggcggaa aaggaaggct acgaggtgcg catcctcacc      420
   gcggaaccgg acctttacca gcttctttcg gagcgaatct ccataccttca cccggagggt      480
   tacctgatca ccccgagtg gctttgggag aagtatgggc ttaagccttc ccagtgggtg      540
   gactaccggg ccttggccgg ggacccttcc gacaacatcc ccggcgtgaa gggcatcggg      600
40gagaagacgg cgccaagct gatccgggag tggggaagcc tggaaaacct tcttaagcac      660
   ctggaacagg tgaaacctgc ctccgtgcgg gagaagatcc ttagccacat ggaggacctc      720
   aagctatccc tggagctatc ccgggtgcgc acggacttgc cccttcaggt ggacttcgcc      780
   cggcgccggg agccggaccg ggaggggctt aaggcctttt tggagaggct ggagttcgga      840
   agcctcctcc acgagttcgg cctgttgaa agcccggtgg cggcggagga agctccctgg      900

```

ccgccccccg	agggagcctt	cgtgggggtac	gttcttttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgcttgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
gccctgaggg	aagggattgc	cctggcaccg	ggcgacgacc	ccatgtctct	cgcctacctc	1140
5ctggatcctt	ccaacaccgc	ccccgaagg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gttgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	ccttttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	cggttgatg	tggcctactt	aaaggccctt	1380
tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	cctggccggg	1440
10catcctttca	acctgaactc	ccgggaccag	ctggaaagg	tcctctttga	cgagcttggg	1500
cttcccgcga	tgggaagac	ggagaagacg	ggcaagcgct	ccaccagcgc	cgccgttttg	1560
gaggccttgc	gggaggctca	tcccatcggt	gaccgcatcc	ttcagtaccg	ggagctttcc	1620
aagctcaagg	gaacctacat	cgatcccttg	cctgccctgg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
15aacctgcaaa	atatccccgt	gcgcacccct	ttggggccagc	ggatccgccg	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtgggtttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctaatc	cggttcttcc	aggagggcca	ggacatccac	1920
accagacgg	ccagctggat	gttcggcggt	ccccagagg	ccgtggattc	cctgatgcgt	1980
cgggcggcca	agaccatcaa	cttcggcggt	ctctacggca	tgtccgcccc	cgggctttcg	2040
20ggagagctgg	ccatccccta	cgaggaggcg	gtggccttca	tcgagcggtg	tttccagagc	2100
taccccaagg	tgcgggcctg	gattgagaaa	accctggcgg	aaggacggga	acggggctat	2160
gtggaacccc	tctttggccg	ccggcgctac	gtgcccgaact	tggcttcccg	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
25cttttgcagg	tgcacgacga	actggctctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gccagggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
gaagtgggca	tcggggagga	ctggctttcc	gccaaaggcct	ag		2502

&lt;210&gt; 2

30&lt;211&gt; 2507

&lt;212&gt; DNA

<213> *Thermus scotoductus*

&lt;400&gt; 2

35atgagggcga	tgctgcccct	ctttgagccc	aagggccggg	tgcttctggt	ggacggccac	60
cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
gtccaggcgg	tgtacgggtt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
gtggtgatcg	tgggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacgaggcc	240
tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
40gagatggtgg	accttttggg	cctggagcgc	ctcgaagtgc	cgggttttga	ggcggatgac	360
gtcctggcca	ccctggccaa	gaaggcggaa	aaggaaggct	acgaggtgcg	catcctcacc	420
gcggaccggg	acctttacca	gcttctttcg	gaccgaatct	ccatccttca	cccggagggt	480

tacctgatca	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
5aagctatccc	tggagctttc	ccgggtgcac	acggagttgc	cccttcaggt	ggacttcgcc	780
cggcgccggg	agccggaccg	ggaagggctt	aaggcctttt	tggagagggt	ggagttcgga	840
agcctcctcc	acgagttcgg	cctgttgga	agcccgggtg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtggggtag	gttctttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
10gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
gccctgaggg	aagggtattg	cctggcacag	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagagggt	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcgg	1320
15gtcctggccc	acatggaggc	cacgggggta	tggttggatg	tggcctactt	gaaggccctt	1380
tccctggagg	tggaggcgga	gctcaggcgc	ctcaggaggg	aggtccaccg	actggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagcttggg	1500
cttcccgcga	tcggcaagac	ggagaagacg	ggtaagcggt	ccaccagcgc	cgccgttttg	1560
gaggctttga	gggagggtca	tcccatagtg	gaccgcatcc	tccagtaccg	ggagctttcc	1620
20aagctcaagg	gaacgtacat	cgatcccttg	cccgcccttg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcgatccc	1740
aacctgcaaa	atatccccgt	gcgcaccctt	ttaggccagc	ggatccgccg	ggccttcgtg	1800
gccgaggagg	ggtggagggt	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagagggccca	ggacatccac	1920
25acccagacgg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggcgctc	ctctacggca	tgtccgccca	ccggctttcg	2040
ggagagctgg	ccatccccta	cgaggaagcg	gtggccttca	tcgagcggtg	tttccagagc	2100
taccccaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
gtggaacccc	tctttggccg	ccggcgctat	gtgcccgaact	tggcttcccg	ggtgaagagc	2220
30atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgagg	tgcacgacga	actggtcctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaaggtgcc	cctggagggtg	2460
gaggtgggta	tcggggagga	ctggctttcc	gccaaggcct	agtcgac		2507

35

&lt;210&gt; 3

&lt;211&gt; 2507

&lt;212&gt; DNA

<213> *Thermus scotoductus*

40

&lt;400&gt; 3

atgagggcga	tgtgtcccct	ctttgagccc	aagggccggg	tgtttctggt	ggacggccac	60
------------	------------	------------	------------	------------	------------	----

	cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
	gtccaggcgg	tgtacgggtt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
	gtggtgatcg	tgggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacgaggcc	240
	tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
5	gagatggtgg	accttttggg	cctggagcgc	ctcgaagtgc	cgggttttga	ggcggatgac	360
	gtcctggcca	ccctggccaa	gaaggcggaa	aaggaaggct	acgaggtgcg	catcctcacc	420
	gcggaaccgg	acctttacca	gcttctttcg	gaccgaatct	ccatccttca	cccggagggg	480
	tacctgatta	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
	gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
10	gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
	ctggaacagg	tgaaacctgc	ctccgtgctg	gagaagatcc	ttagccacat	ggaggacctc	720
	aagctatccc	tggagctttc	ccgggtgcac	acggagttgc	cccttcaggt	ggacttcgcc	780
	cggcgccggg	agccggaccg	ggaagggtct	aaggcctttt	tggagaggct	ggagttcgga	840
	agcctcctcc	acgagttcgg	cctgttgga	agcccgggtg	cggcgaggga	agctccctgg	900
15	ccgccccccg	agggagcctt	cgtgggggtac	gttctttccc	gccccgagcc	catgtgggcg	960
	gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
	gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
	gccctgaggg	aagggttgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
	ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
20	gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
	cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
	gtcctggccc	acatggaggc	cacgggggta	tgggttgatg	tggcctactt	gaaggccctt	1380
	tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	actggccggg	1440
	catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagcttggg	1500
25	cttcccccca	tcggcaagac	ggagaagacg	ggtaagcgtt	ccaccagcgc	cgcggttttg	1560
	gaggctttga	gggaggctca	tcccatagtg	gaccgcatcc	tccagtaccg	ggagctttcc	1620
	aagctcaagg	gaacgtacat	cgatcccttg	cccgccttgg	tccaccccaa	gacgaaccgc	1680
	ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
	aacctgcaaa	atatccccgt	gcgcaccctt	ttaggccagc	ggatccgccc	ggccttcgtg	1800
30	gccgaggagg	ggtggaggct	ggtgggtttg	gactacagcc	agattgagct	cagggtcctg	1860
	gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagagggcca	ggacatccac	1920
	accagacgg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
	cgggcggcca	agaccatcaa	ctacggcgtc	ctctacggca	tgtccgcccc	ccggctttcg	2040
	ggagagctgg	ccatccccta	cgagggaagcg	gtggccttca	tcgagcggtg	tttccagagc	2100
35	ttcccccaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
	gtggaaaccc	tctttggccg	ccggcgctat	gtgcccgaact	tggcttcccc	ggtgaagagc	2220
	atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgcgcgggat	2280
	ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
	cttttgcagg	tgcacgacga	actggctctc	gaggctccca	aggagcaagc	ggagggaagtc	2400
40	gccagaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
	gaggtgggta	tcggggaggga	ctggctttcc	gccaaggcct	agtcgac		2507

&lt;210&gt; 4

&lt;211&gt; 2502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain X-1, having GAC (encoding Asp) in place of GGG (encoding Gly) at positions 136-138.

10

&lt;400&gt; 4

atgagggcga	tgctgccct	ctttgagccc	aagggccggg	tgcttctggt	ggacggccac	60
cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
gtccaggcgg	tgtacgactt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
15gtggtgatcg	tggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacgaggcc	240
tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
gagatggtgg	accttttggg	cctggagcgc	ctcgaggtgc	cgggctttga	ggcggatgac	360
gtcctggcta	ccctggccaa	gaaggcggaa	aaggaaggct	acgaggtgcg	catcctcacc	420
gcggaccggg	acctttacca	gcttctttcg	gagcgaatct	ccatccttca	cccggagggt	480
20tacctgatca	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
aagctatccc	tggagctatc	ccgggtgcgc	acggacttgc	cccttcaggt	ggacttcgcc	780
25cggcgccggg	agccggaccg	ggaggggctt	aaggcctttt	tggagaggct	ggagtccgga	840
agcctcctcc	acgagttcgg	cctgttgga	agcccggtgg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtggggtag	gttctttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgcttgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
30gccctgaggg	aagggttgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gttgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	cggttggatg	tggcctactt	aaaggccctt	1380
35tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	cctggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagcttggg	1500
cttcccgcga	tcggcaagac	ggagaagacg	ggcaagcgct	ccaccagcgc	cgcggttttg	1560
gaggccttgc	gggaggctca	tcccatcggt	gaccgcatcc	ttcagtaccg	ggagctttcc	1620
aagctcaagg	gaacctacat	cgatcccttg	cctgcccttg	tccaccccaa	gacgaaccgc	1680
40ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
aacctgcaaa	atatccccgt	gcgcacccct	ttgggccagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860

```

gcgcaccttt ccggggacga gaacctaatc cgggtcttcc aggagggcca ggacatccac 1920
accagacg ccagctggat gttcggcgtg ccccgagagg ccgtggattc cctgatgcgt 1980
cgggcggcca agaccatcaa ctccggcgtc ctctacggca tgtccgcca ccggctttcg 2040
ggagagctgg ccatccccta cgaggaggcg gtggccttca tcgagcggtt tttccagagc 2100
5taccccaagg tgcgggcctg gattgagaaa accctggcgg aaggacggga acggggctat 2160
gtggaacccc tctttggccg ccggcgctac gtgcccgact tggcttccc ggtgaagagc 2220
atccgggagg cagcggagcg catggccttc aacatgccgg tccaggggac cgccgcggat 2280
ttgatgaaac tggccatggt gaagctcttt cccaggcttc aggagctggg ggccaggatg 2340
cttttgcagg tgcacgacga actggctctc gaggtctcca aggagcaagc ggaggaagtc 2400
10gccaggagg ccaagcggac catggaggag gtgtggcccc tgaagggtgc cttggagggtg 2460
gaagtgggca tcggggagga ctggctttcc gccaaaggcct ag 2502

```

<210> 5

<211> 2507

15<212> DNA

<213> Artificial Sequence

<220>

20 <223> A derivative nucleic acid related to *Thermus scotoductus*, strain SM3, having GAC (encoding Asp) in place of GGG (encoding Gly) at positions 136-138.

<400> 5

```

atgagggcga tgctgccctt ctttgagccc aagggccggg tgcttctggt ggacggccac 60
25cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg 120
gtccaggcgg tgtacgactt tgccaagagc cttttgaagg cgctaaggga agacggggat 180
gtggtgatcg tgggttttga cgccaaggcc ccctccttcc gccaccagac ctacgaggcc 240
tacaaggcgg ggccgggtcc ccccccgag gactttcccc ggcagcttgc cttatcaag 300
gagatggtgg accttttggg cctggagcgc ctccaagtgc cgggttttga ggcggatgac 360
30gtcctggcca ccctggccaa gaagcgggaa aaggaaggct acgaggtgcg catcctcacc 420
gcggaaccgg acctttacca gcttctttcg gaccgaatct ccctccttca cccggagggt 480
tacctgatca ccccgagtg gctttgggag aagtatgggc ttaagccttc ccagtgggtg 540
gactaccggg ccttggccgg ggacccttcc gacaacatcc ccggcgtgaa gggcatcggg 600
gagaagacgg cggccaagct gatccgggag tggggaagcc tggaaaacct tcttaagcac 660
35ctggaacagg tgaaacctgc ctccgtgcgg gagaagatcc ttagccacat ggaggacctc 720
aagctatccc tggagctttc ccgggtgcac acggagttgc cccttcaggt ggacttcgcc 780
cggcgccggg agccggaccg ggaagggtct aaggcctttt tggagaggct ggagttcgga 840
agcctcctcc acgagttcgg cctgttgga agccgggtgg cggcgaggga agctccctgg 900
ccgccccccg agggagcctt cgtgggttac gttctttccc gccccgagcc catgtgggcg 960
40gagcttaacg ccttgccgcg cgcctgggag ggaagggttt accgggcgga ggatcccttg 1020
gaggccttgc gggggcttgg ggaggtgagg gggcttttgg ccaaggacct ggcggtgctg 1080
gccctgaggg aagggttgc cctggcacag ggcgacgacc ccattgctct cgcctacctc 1140

```

ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	tggttggatg	tggcctactt	gaaggccctt	1380
5tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	actggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagcttggg	1500
cttcccgcca	tcggcaagac	ggagaagacg	ggtaagcggt	ccaccagcgc	cgccgttttg	1560
gaggctttga	gggaggctca	tcccatagt	gaccgcatcc	tccagtaccg	ggagctttcc	1620
aagctcaagg	gaacgtacat	cgatcccttg	cccgccctgg	tccaccccaa	gacgaaccgc	1680
10ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
aacctgcaaa	atatccccgt	gcgcaccctt	ttaggccagc	ggatccgccg	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagaggggca	ggacatccac	1920
accagacg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
15cgggcggcca	agaccatcaa	cttcggcgtc	ctctacggca	tgtccgcccc	ccggttttcg	2040
ggagagctgg	ccatccccta	cgaggaagcg	gtggccttca	tcgagcggta	tttccagagc	2100
tacccaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
gtggaacccc	tctttggccg	ccggcgctat	gtgcccgact	tggcttcccg	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
20ttgatgaaac	tggccatggg	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgcagg	tgcacgacga	actggtcctc	gaggtccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaaggtgcc	cttggagggtg	2460
gagggtgggta	tcggggagga	ctggctttcc	gccaaggcct	agtcgac		2507

25&lt;210&gt; 6

&lt;211&gt; 2507

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

30&lt;220&gt;

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain Vi7a, having GAC (encoding Asp) in place of GGG (encoding Gly) at positions 136-138.

35&lt;400&gt; 6

atgaggggcga	tgctgcccct	ctttgagccc	aaggggccggg	tgcttctggt	ggacggccac	60
cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
gtccaggcgg	tgtacgactt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
gtggtgatcg	tgggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacagggcc	240
40tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
gagatggtgg	accttttggg	cctggagcgc	ctcgaagtgc	cgggttttga	ggcggatgac	360
gtcctggcca	ccctggccaa	gaaggcggaa	aaggaaggct	acgaggtgcg	catcctcacc	420

gcggaccggg	acctttacca	gcttctttcg	gaccgaatct	ccatccttca	cccggagggt	480
tacctgatta	ccccggagt	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
5ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
aagctatccc	tggagctttc	ccgggtgcac	acggagtgtc	cccttcaggt	ggacttcgcc	780
cggcgccggg	agccggaccg	ggaagggctt	aaggcctttt	tggagaggct	ggagttcgga	840
agcctcctcc	acgagttcgg	cctgttgga	agcccgggtg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtgggggtac	gttctttccc	gccccgagcc	catgtgggcg	960
10gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
gccctgaggg	aagggtattg	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaagg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
15cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	tggttggatg	tggcctactt	gaaggccctt	1380
tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	actggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaagg	tcctctttga	cgagcttggg	1500
cttcccccca	tgcgcaagac	ggagaagacg	ggtaagcggt	ccaccagcgc	cgcggttttg	1560
20gaggctttga	gggagggtca	tcccatagtg	gaccgcatcc	tccagtaccg	ggagctttcc	1620
aagctcaagg	gaacgtacat	cgatcccttg	cccgccttgg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggtatccc	1740
aacctgcaaa	atatccccgt	gcgcacccct	ttagggcagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggagggt	ggtgggtttg	gactacagcc	agattgagct	cagggtcctg	1860
25gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagagggccca	ggacatccac	1920
accagacggg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	ctacggcgtc	ctctacggca	tgtccgcccc	ccggctttcg	2040
ggagagctgg	ccatccccta	cgaggaagcg	gtggccttca	tcgagcggtg	tttccagagc	2100
ttccccaaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
30gtggaaaccc	tctttggccg	ccggcgctat	gtgcccgaact	tggcttccc	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgcagg	tgcacgacga	actggctctc	gaggctccca	aggagcaagc	ggagggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
35gaggtgggta	tgcgggagga	ctggctttcc	gccaaaggcct	agtcgac		2507



&lt;210&gt; 7

&lt;211&gt; 2502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain X-1, having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2002-04.

10

&lt;400&gt; 7

atgagggcga	tgctgcccct	ctttgagccc	aagggccggg	tgcttctggt	ggacggccac	60
cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
gtccaggcgg	tgtacggggt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
15gtggtgatcg	tggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacgaggcc	240
tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
gagatggtgg	accttttggg	cctggagcgc	ctcgagggtg	cgggctttga	ggcggatgac	360
gtcctggcta	ccctggccaa	gaaggcggaa	aaggaaggct	acgagggtgc	catcctcacc	420
gcggaaccgg	acctttacca	gcttctttcg	gagcgaatct	ccatccttca	cccggagggt	480
20tacctgatca	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
aagctatccc	tggagctatc	ccgggtgcgc	acggacttgc	cccttcaggt	ggacttcgcc	780
25cggcgccggg	agccggaccg	ggaggggctt	aaggcctttt	tggagaggct	ggagttcgga	840
agcctcctcc	acgagttcgg	cctgttggaa	agcccgggtg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtgggggtac	gttctttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggggga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
30gccctgaggg	aagggattgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gtacgggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gttgctttcc	gaaaggcttt	acgcgcacct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	cggttggatg	tggcctactt	aaaggccctt	1380
35tccctggagg	tggaggcgga	gtcaggcgc	ctcgaggagg	aggtccaccg	cctggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tctcttttga	cgagcttggg	1500
cttcccgcga	tggcaagac	ggagaagacg	ggcaagcgct	ccaccagcgc	cgcggttttg	1560
gaggccttgc	gggaggctca	tcccatcgtg	gaccgcatec	ttcagtaccg	ggagctttcc	1620
aagctcaagg	gaacctacat	cgatcccttg	cctgcccttg	tccaccccaa	gacgaaccgc	1680
40ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
aacctgcaaa	atatccccgt	gcgcacccct	ttgggccagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860

```

gcgcaccttt ccggggacga gaacctaatc cgggtcttcc aggagggcca ggacatccac 1920
accagacgg ccagctggat gttcggcgtg ccccagagg ccgtggattc cctgatgcgt 1980
cgggcggcca agaccatcaa ctacggcgtc ctctacggca tgtccgcca ccggctttcg 2040
ggagagctgg ccatccccta cgaggaggcg gtggccttca tcgagcggta tttccagagc 2100
5taccccaagg tgcgggcctg gattgagaaa accctggcgg aaggacggga acggggctat 2160
gtggaacccc tctttggccg ccggcgctac gtgcccact tggcttccc ggtgaagagc 2220
atccgggagg cagcggagcg catggccttc aacatgccgg tccaggggac cgcgcggat 2280
ttgatgaaac tggccatggt gaagctcttt ccaggcttc aggagctggg ggccaggatg 2340
cttttgcagg tgcacgacga actggtcctc gaggctccca aggagcaagc ggaggaagtc 2400
10gcccaggagg ccaagcggac catggaggag gtgtggcccc tgaagggtgc cttggagggtg 2460
gaagtgggca tcggggagga ctggctttcc gccaaggcct ag 2502

```

<210> 8

<211> 2507

15<212> DNA

<213> Artificial Sequence

<220>

20 <223> A derivative nucleic acid related to *Thermus scotoductus*, strain SM3, having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2002-04.

<400> 8

```

atgagggcga tgctgcccct ctttgagccc aagggccggg tgcttctggt ggacggccac 60
25cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg 120
gtccaggcgg tgtacgggtt tgccaagagc cttttgaagg cgctaaggga agacggggat 180
gtggtgatcg tgggttttga cgccaaggcc cctccttcc gccaccagac ctacgaggcc 240
tacaaggcgg ggcgggctcc ccccccgag gactttcccc ggcagcttgc ccttatcaag 300
gagatggtgg accttttggg cctggagcgc ctgcaagtgc cgggttttga ggcggatgac 360
30gtcctggcca ccctggccaa gaaggcggaa aaggaaggct acgaggtgcg catcctcacc 420
gcggaccggg acctttacca gcttctttcg gaccgaatct ccaccttca cccggagggt 480
tacctgatca ccccgagtg gctttgggag aagtatgggc ttaagccttc ccagtgggtg 540
gactaccggg ccttggccgg ggacccttcc gacaacatcc ccggcgtgaa gggcatcggg 600
gagaagacgg cggccaagct gatccgggag tggggaagcc tggaacacct tcttaagcac 660
35ctggaacagg tgaaacctgc ctccgtgcgg gagaagatcc ttagccacat ggaggacctc 720
aagctatccc tggagctttc ccgggtgcac acggagttgc cccttcaggt ggacttcgcc 780
cggcgccggg agccggaccg ggaagggtt aaggcctttt tggagaggct ggagttcgga 840
agcctcctcc acgagttcgg cctgttgga agcccgggtg cggcgaggga agctccctgg 900
ccgccccccg agggagcctt cgtgggggtac gttctttccc gccccgagcc catgtgggcg 960
40gagcttaacg ccttgccgc cgcctgggag ggaagggttt accgggcgga ggatcccttg 1020
gaggccttgc gggggcttgg ggaggtgagg gggcttttgg ccaaggacct ggcgggtgctg 1080
gccctgaggg aagggttgc cctggcacag ggcgacgacc ccatgctcct cgcctacctc 1140

```

```

ctggatcctt ccaacaccgc ccccgagggt gtagcccgcc gctacggggg ggagtggacc 1200
gaggaggcgg gggaaaggcc gctgctttcc gaaaggcttt acgccgccct cctggagcgg 1260
cttaaggggg aggagaggct tctttggctt tacgaggagg tggaaaagcc cctttcgcg 1320
gtcctggccc acatggaggc cacgggggta tggttggatg tggcctactt gaaggccctt 1380
5tccctggagg tggaggcggg gctcaggcgc ctcgaggagg aggtccaccg actggccggg 1440
catcctttca acctgaactc ccgggaccag ctggaaaggg tcctctttga cgagcttggg 1500
cttcccggca tcggcaagac ggagaagacg ggtaagcgtt ccaccagcgc cgccgttttg 1560
gaggctttga gggaggctca tcccatagt gaccgcatcc tccagtaccg ggagctttcc 1620
aagctcaagg gaacgtacat cgatcccttg ccgcccttg tccaccccaa gacgaaccgc 1680
10ctccacaccc gtttcaacca gacggccacc gccacgggga ggcttagcag ctccgatccc 1740
aacctgcaaa atatccccgt gcgcacccct ttaggccagc ggatccgccg ggccttcgtg 1800
gccgaggagg ggtggaggct ggtggttttg gactacagcc agattgagct cagggtcctg 1860
gcgcaccttt ccggggacga gaacctgatc cgggtcttcc aagagggcca ggacatccac 1920
accagacgag ccagctggat gttcggcgtg cccccagagg ccgtggattc cctgatgcgc 1980
15cgggcggcca agaccatcaa ctacggcgtc ctctacggca tgtccgcccc ccggctttcg 2040
ggagagctgg ccatccccct cgaggaagcg gtggccttca tcgagcggta tttccagagc 2100
taccccaagg tacgggcctg gattgagaaa accctggcgg aaggacggga gcggggctat 2160
gtggaacccc tctttggccg ccggcgctat gtgcccact tggcttcccg ggtgaagagc 2220
atccgggagg cagcggagcg catggccttc aacatgccgg tccaggggac cgccgcggat 2280
20ttgatgaaac tggccatggt gaagctcttt cccaggcttc aggagctggg ggccaggatg 2340
cttttgcaag tgcacgacga actggtcctc gaggctccca aggagcaagc ggaggaagtc 2400
gcccaggagg ccaagcggac catggaggag gtgtggcccc tgaaggtgcc cttggagggtg 2460
gagggtgggt tccggggagg ctggctttcc gccaaaggcct agtcgac 2507

```

25<210> 9

<211> 2507

<212> DNA

<213> Artificial Sequence

30<220>

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain Vi7a, having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2101-03.

35<400> 9

```

atgaggggcga tgctgcccct ctttgagccc aaggggccggg tgcttctggt ggacggccac 60
cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg 120
gtccaggcgg tgtacgggtt tgccaagagc cttttgaagg cgctaaggga agacggggat 180
gtggtgatcg tgggttttga cgccaaggcc ccctccttcc gccaccagac ctacagggcc 240
40tacaaggcgg ggcgggctcc ccccccgag gactttcccc ggcagcttgc ctttatcaag 300
gagatggttg accttttggg cctggagcgc ctcgaagtgc cgggttttga ggccgatgac 360
gtcctggcca ccctggccaa gaaggcggaa aagggaaggct acgaggtgcg catcctcacc 420

```

	gcggaaccggg	acctttacca	gcttctttcg	gaccgaatct	ccatccttca	cccggagggt	480
	tacctgatta	ccccggagt	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
	gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
	gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
5	ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
	aagctatccc	tggagctttc	ccgggtgcac	acggagtgtc	cccttcaggt	ggacttcgcc	780
	cggcgccggg	agccggaccg	ggaagggtct	aaggcctttt	tggagaggct	ggagttcgga	840
	agcctcctcc	acgagttcgg	cctgttgga	agcccgggtg	cggcggagga	agctccctgg	900
	ccgccccccg	agggagcctt	cgtgggggtac	gttctttccc	gccccgagcc	catgtgggcg	960
10	gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
	gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
	gccctgaggg	aagggtattg	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
	ctggatcctt	ccaacaccgc	ccccgaagg	gtagcccggc	gctacggggg	ggagtggacc	1200
	gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgcctt	cctggagcgg	1260
15	cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
	gtcctggccc	acatggaggc	cacgggggta	tggttggatg	tggcctactt	gaaggccctt	1380
	tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	actggccggg	1440
	catcctttca	acctgaactc	ccgggaccag	ctggaaagg	tcctctttga	cgagcttggg	1500
	cttcccgcga	tcggcaagac	ggagaagacg	ggtaagcggt	ccaccagcgc	cgccgttttg	1560
20	gaggctttga	gggaggctca	tcccatagt	gaccgcatcc	tccagtaccg	ggagctttcc	1620
	aagctcaagg	gaacgtacat	cgatcccttg	cccgccctgg	tccaccccaa	gacgaaccgc	1680
	ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
	aacctgcaaa	atatccccgt	gcgcaccctt	ttaggccagc	ggatccgccc	ggccttcgtg	1800
	gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
25	gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagagggcca	ggacatccac	1920
	accagacgg	ccagctggat	gttcggcggt	ccccagagg	ccgtggattc	cctgatgcgc	1980
	cgggcggcca	agaccatcaa	ctacggcgtc	ctctacggca	tgtccgccc	ccggctttcg	2040
	ggagagctgg	ccatccccta	cgaggaagcg	gtggccttca	tcgagcggt	tttccagagc	2100
	tacccaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
30	gtggaaaccc	tctttggccg	ccggcgctat	gtgcccgact	tggcttccc	ggtgaagagc	2220
	atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
	ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
	cttttgacag	tgcacgacga	actggtcctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
	gccagaggag	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
35	gaggtgggta	tcggggagga	ctggctttcc	gccaaaggcct	agtcgac		2507

&lt;210&gt; 10

&lt;211&gt; 2502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain X-1, having GAC (encoding Asp) in place of GGG (encoding Gly) at positions 136-138 and having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2002-04.

10

&lt;400&gt; 10

atgagggcga	tgctgccct	ctttgagccc	aagggccggg	tgtttctggt	ggacggccac	60
cacctggcct	accgtacctt	ttttgccctg	aagggcctca	ccaccagccg	cggggagccg	120
15gtccaggcgg	tgtacgactt	tgccaagagc	cttttgaagg	cgctaaggga	agacggggat	180
gtggtgatcg	tggtgtttga	cgccaaggcc	ccctccttcc	gccaccagac	ctacgaggcc	240
tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
gagatggtgg	accttttggg	cctggagcgc	ctcgagggtg	cgggctttga	ggcggatgac	360
gtcctggcta	ccctggccaa	gaaggcggaa	aaggaaggct	acgagggtgc	catcctcacc	420
20gcggaccggg	acctttacca	gcttctttcg	gagcgaatct	ccatccttca	cccggagggt	480
tacctgatca	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
25aagctatccc	tggagctatc	ccgggtgcgc	acggacttgc	cccttcaggt	ggacttcgcc	780
cggcgccggg	agccggaccg	ggaggggctt	aaggcctttt	tggagaggct	ggagttcgga	840
agcctcctcc	acgagttcgg	cctgttgga	agcccgggtg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtggggtag	gttctttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgcctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
30gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
gccctgaggg	aagggattgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gttgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
35gtcctggccc	acatggaggc	cacgggggta	cggttggtg	tggcctactt	aaaggccctt	1380
tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	cctggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagcttggg	1500
cttcccgcga	tcggcaagac	ggagaagacg	ggcaagcgct	ccaccagcgc	cgccttttg	1560
gaggccttgc	gggaggetca	tcccatcggt	gaccgcatcc	ttcagtaccg	ggagctttcc	1620
40aagctcaagg	gaacctacat	cgatcccttg	cctgccctgg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
aacctgcaaa	atatccccgt	gcgcaccctt	ttgggcccag	ggatccgccg	ggccttcgtg	1800

```

gccgaggagg ggtggaggct ggtgggtttt gactacagcc agattgagct cagggtcctg 1860
gcgcaccttt ccggggacga gaacctaatc cgggtcttcc aggagggcca ggacatccac 1920
acccagacgg ccagctggat gttcggcgtg ccccagagg ccgtggattc cctgatgcgt 1980
cgggcggcca agaccatcaa ctacggcgtc ctctacggca tgtccgcca ccggctttcg 2040
5ggagagctgg ccatccccta cgaggaggcg gtggccttca tcgagcggta tttccagagc 2100
taccccaagg tgcgggcctg gattgagaaa accctggcgg aaggacggga acggggctat 2160
gtggaaaccc tctttggcgg ccggcgctac gtgcccgact tggcttcccg ggtgaagagc 2220
atccgggagg cagcggagcg catggccttc aacatgccgg tccaggggac cgccgcggat 2280
ttgatgaaac tggccatggt gaagctcttt ccaggcttc aggagctggg ggccaggatg 2340
10cttttgcagg tgcacgacga actggtcctc gaggtccca aggagcaagc ggaggaagtc 2400
gcccaggagg ccaagcggac catggaggag gtgtggcccc tgaagggtgcc cttggagggtg 2460
gaagtgggca tcggggagga ctggctttcc gccaggcct ag 2502

```

<210> 11

15<211> 2507

<212> DNA

<213> Artificial Sequence

<220>

20<223> A derivative nucleic acid related to *Thermus scotoductus*, strain SM3, having GAC (encoding Asp) place of GGG (encoding Gly) at positions 136-138 and having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2002-04.

25<400> 11

```

atgagggcga tgetgcccct ctttgagccc aagggccggg tgcttctggt ggacggccac 60
cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg 120
gtccaggcgg tgtacgactt tgccaagagc cttttgaagg cgctaaggga agacggggat 180
gtggtgatcg tgggtgttga cgccaaggcc ccctccttcc gccaccagac ctacgaggcc 240
30tacaaggcgg ggcgggctcc cacccccag gactttccc ggagcttgc ctttatcaag 300
gagatggtgg accttttggg cctggagcgc ctcgaagtgc cgggttttga ggcgatgac 360
gtcctggcca ccctggccaa gaaggcggaa aaggaaggct acgaggtgcg catcctcacc 420
gcggaccggg acctttacca gttcttttcg gaccgaatct ccctccttca cccggagggt 480
tacctgatca ccccgagtg gctttgggag aagtatgggc ttaagccttc ccagtgggtg 540
35gactaccggg ccttggccgg ggacccttcc gacaacatcc ccggcgtgaa gggcatcggg 600
gagaagacgg cggccaagct gatccgggag tggggaagcc tggaaaacct tcttaagcac 660
ctggaacagg tgaaacctgc ctccgtgcgg gagaagatcc ttagccacat ggaggacctc 720
aagctatccc tggagctttc ccgggtgcac acggagttgc cccttcaggt ggacttcgcc 780
cggcgccggg agccggaccg ggaagggtt aaggcctttt tggagaggct ggagttcgga 840
40agcctcctcc acgagttcgg cctgttgaa agcccggtgg cggcgaggga agctccctgg 900
ccgccccccg agggagcctt cgtgggggtac gttctttccc gccccgagcc catgtgggcg 960
gagcttaacg ccttggccgc cgcctgggag ggaagggttt accgggcgga ggatcccttg 1020

```

gaggccttgc gggggccttg ggaggtgagg gggccttttg ccaaggacct ggcggtgctg 1080  
 gccctgaggg aagggtattgc cctggcacag ggcgacgacc ccatgtctct cgcctacctc 1140  
 ctggatcctt ccaacaccgc cccgaagggt gtagcccggt gctacggggg ggagtggacc 1200  
 gaggaggcgg gggaaagggc gctgctttcc gaaaggcttt acgccgccct cctggagcgg 1260  
 5cttaagggg aggagaggct tctttggctt tacgaggagg tggaaaagcc cctttcgcg 1320  
 gtcctggccc acatggaggc cacgggggta tggttggatg tggcctactt gaaggccctt 1380  
 tccctggagg tggaggcggg gctcaggcgc ctcgaggagg aggtccaecg actggccggg 1440  
 catcctttca acctgaactc ccgggaccag ctggaaaggg tcctctttga cgagcttggg 1500  
 cttcccgcga tcggcaagac ggagaagacg ggtaagcggt ccaccagcgc cgccgttttg 1560  
 10gaggccttga gggaggctca tcccatagt gaccgcatcc tccagtaccg ggagccttcc 1620  
 aagctcaagg gaacgtacat cgatcccttg cccgccctgg tccacccaa gacgaaccgc 1680  
 ctccacaccc gtttcaacca gacggccacc gccacgggga ggcttagcag ctcggtatccc 1740  
 aacctgcaaa atatccccgt gcgcacccct ttaggccagc ggatccgccg ggccttcgtg 1800  
 gccgaggagg ggtggaggct ggtgggtttg gactacagcc agattgagct cagggtcctg 1860  
 15gcgcaccttt ccggggacga gaacctgatc cgggtcttcc aagagggcca ggacatccac 1920  
 acccagacgg ccagctggat gttcggcggt cccccagagg ccgtggattc cctgatgcgc 1980  
 cgggcgccca agaccatcaa ctacggcgct ctctacggca tgtccgcccc ccggttttcg 2040  
 ggagagctgg ccatccccta cgaggaagcg gtggccttca tcgagcggtt tttccagagc 2100  
 taccccaagg tacgggcctg gattgagaaa accctggcgg aaggacggga gcggggctat 2160  
 20gtggaacccc tctttggccg ccggcgctat gtgcccact tggcttccc ggtgaagagc 2220  
 atccgggagg cagcggagcg catggccttc aacatgccgg tccaggggac cgccgcggat 2280  
 ttgatgaaac tggccatggt gaagctcttt ccaggcttc aggagctggg ggccaggatg 2340  
 cttttgcagg tgcacgacga actggtcctc gaggtccca aggagcaagc ggaggaagtc 2400  
 gcccaggagg ccaagcggac catggaggag gtgtggcccc tgaagggtgc cttggagggtg 2460  
 25gaggtgggta tcggggagga ctggctttcc gccaaaggcct agtcgac 2507

<210> 12

<211> 2507

<212> DNA

30<213> Artificial Sequence

<220>

<223> A derivative nucleic acid related to *Thermus scotoductus*, strain Vi7a, having GAC (encoding Asp) in place of GGG (encoding Gly) at positions 136-138 and having TAC (encoding Tyr) in place of TTC (encoding Phe) at positions 2101-03.

<400> 12

atgagggcga tgctgcccct ctttgagccc aagggccggg tgcttctggt ggacggccac 60  
 40cacctggcct accgtacctt ttttgccctg aagggcctca ccaccagccg cggggagccg 120  
 gtccaggcgg tgtacgactt tgccaagagc cttttgaagg cgctaaggga agacggggat 180  
 gtggtgatcg tgggttttga cgccaaggcc ccctccttcc gccaccagac ctacagggcc 240

tacaaggcgg	ggcgggctcc	cacccccgag	gactttcccc	ggcagcttgc	ccttatcaag	300
gagatggtgg	accttttggg	cctggagcgc	ctcgaagtgc	cgggttttga	ggcggatgac	360
gtcctggcca	ccctggccaa	gaaggcggaa	aaggaaggct	acgaggtgcg	catcctcacc	420
gcggaaccggg	acctttacca	gcttctttcg	gaccgaatct	ccatccttca	cccggaggggt	480
5tacctgatta	ccccggagtg	gctttgggag	aagtatgggc	ttaagccttc	ccagtgggtg	540
gactaccggg	ccttggccgg	ggacccttcc	gacaacatcc	ccggcgtgaa	gggcatcggg	600
gagaagacgg	cggccaagct	gatccgggag	tggggaagcc	tggaaaacct	tcttaagcac	660
ctggaacagg	tgaaacctgc	ctccgtgcgg	gagaagatcc	ttagccacat	ggaggacctc	720
aagctatccc	tggagctttc	ccgggtgcac	acggagtgtc	cccttcaggt	ggacttcgcc	780
10cggcgccggg	agccggaccg	ggaagggtct	aaggcctttt	tggagaggct	ggagttcgga	840
agcctcctcc	acgagttcgg	cctgttgga	agcccgttg	cggcggagga	agctccctgg	900
ccgccccccg	agggagcctt	cgtgggggtac	gttctttccc	gccccgagcc	catgtgggcg	960
gagcttaacg	ccttggccgc	cgctgggag	ggaagggttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcgggtgctg	1080
15gccttgagg	aagggtattg	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaagg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggaggcgg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctggagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcg	1320
gtcctggccc	acatggaggc	cacgggggta	tggttggatg	tggcctactt	gaaggccctt	1380
20tccctggagg	tggaggcgga	gctcaggcgc	ctcgaggagg	aggtccaccg	actggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaagg	tcctctttga	cgagcttggg	1500
cttcccgcga	tgggcaagac	ggagaagacg	ggtaagcgtt	ccaccagcgc	cgccgttttg	1560
gaggctttga	gggaggctca	tcccatagt	gaccgcaccc	tccagtaccg	ggagctttcc	1620
aagctcaagg	gaacgtacat	cgatcccttg	ccgcgccctg	tccaccccaa	gacgaaccgc	1680
25ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatccc	1740
aacctgcaaa	atatccccgt	gcgacccctt	ttaggccagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctgatc	cgggtcttcc	aagaggggcca	ggacatccac	1920
accagacgg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
30cggggcgcca	agaccatcaa	ctacggcgtc	ctctacggca	tgtccgcccc	ccggctttcg	2040
ggagagctgg	ccatccccta	cgaggaagcg	gtggccttca	tcgagcggtg	tttccagagc	2100
taccccaagg	tacgggcctg	gattgagaaa	accctggcgg	aaggacggga	gcggggctat	2160
gtggaacccc	tctttggccg	ccggcgctat	gtgcccgact	tggcttcccc	ggtgaagagc	2220
atccggggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
35ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgcagg	tgcacgacga	actggtcctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
gagggtgggtg	tgggggagga	ctggctttcc	gccaaaggcct	agtcgac		2507



&lt;210&gt; 13

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A wild type *Thermus scotoductus* nucleic acid polymerase polypeptide from strain X-1 with three additional amino acids at the N-terminus.

10&lt;400&gt; 13

Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
15Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
	50					55				60					
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
2065					70				75					80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
				85				90					95		
Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
			100					105				110			
25Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
		115					120					125			
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130					135				140					
Leu	Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly
30145				150				155				160			
Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro
			165					170				175			
Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn
		180						185				190			
35Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile
		195					200				205				
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val
	210				215					220					
Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu
40225				230				235				240			
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Gln
			245					250				255			

Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala			
			260					265					270					
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu			
		275					280					285						
5Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu			
		290				295					300							
Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala			
305					310					315					320			
Glu	Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala			
10				325					330					335				
Glu	Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu			
			340					345					350					
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu			
		355					360					365						
15Ala	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser			
		370				375					380							
Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr			
385					390					395					400			
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala			
20				405					410				415					
Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu			
			420					425					430					
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr			
		435					440					445						
25Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val			
		450				455					460							
Glu	Ala	Glu	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly			
465					470					475					480			
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe			
30				485					490					495				
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys			
			500					505					510					
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro			
		515					520						525					
35Ile	Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly			
		530				535						540						
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg			
545					550					555					560			
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser			
40				565					570				575					
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly			
			580					585					590					

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 5Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 10 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 15Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 20 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 25His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 30 820 825 830  
 Ala

<210> 14

35<211> 830

<212> PRT

<213> Thermus scotoductus

<400> 14

40Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 1 5 10 15

His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu Thr Thr  
 20 25 30  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 35 40 45  
 5Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val Phe Asp  
 50 55 60  
 Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr Lys Ala  
 65 70 75 80  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 10 85 90 95  
 Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val Pro Gly  
 100 105 110  
 Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala Glu Lys  
 115 120 125  
 15Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu Tyr Gln  
 130 135 140  
 Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr Leu Ile  
 145 150 155 160  
 Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser Gln Trp  
 20 165 170 175  
 Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly  
 180 185 190  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg Glu Trp  
 195 200 205  
 25Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys Pro Ala  
 210 215 220  
 Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys Leu Ser  
 225 230 235 240  
 Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Gln Val Asp Phe  
 30 245 250 255  
 Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu  
 260 265 270  
 Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser  
 275 280 285  
 35Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe  
 290 295 300  
 Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn  
 305 310 315 320  
 Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala Glu Asp Pro  
 40 325 330 335  
 Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu Ala Lys  
 340 345 350

	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	Ala	Pro	Gly	
		355						360					365				
	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Ala	
		370					375					380					
5	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	Ala	
		385				390					395				400		
	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	Leu	Leu	Glu	
					405					410				415			
	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val	Glu	
10				420				425				430					
	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	
			435				440					445					
	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala	Glu	
		450				455					460						
15	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	His	Pro	Phe	
		465				470				475					480		
	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	
				485				490				495					
	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr	
20			500					505				510					
	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Asp	
		515				520				525							
	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	Thr	Tyr	Ile	
		530				535				540							
25	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	Leu	His	Thr	
		545				550				555				560			
	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
				565				570				575					
	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	
30			580					585				590					
	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	Val	Leu	Asp	
		595				600				605							
	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	
		610				615				620							
35	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	Thr	Gln	Thr	
		625				630				635				640			
	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Ser	Leu	Met	
				645				650				655					
	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	
40			660					665				670					
	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	
		675				680				685							

Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala	Trp
690						695					700				
Ile	Glu	Lys	Thr	Leu	Ala	Glu	Gly	Arg	Glu	Arg	Gly	Tyr	Val	Glu	Thr
705					710					715				720	
5Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala	Ser	Arg	Val	Lys
				725					730					735	
Ser	Ile	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln
			740					745						750	
Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro
10		755					760					765			
Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp	Glu
		770				775					780				
Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val	Ala	Gln	Glu
785					790					795				800	
15Ala	Lys	Arg	Thr	Met	Glu	Glu	Val	Trp	Pro	Leu	Lys	Val	Pro	Leu	Glu
				805					810					815	
Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Ala		
			820					825					830		

20&lt;210&gt; 15

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

25&lt;400&gt; 15

Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
30Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
		35					40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
		50				55					60				
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
3565					70					75				80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
				85					90					95	
Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
			100					105					110		
40Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
			115					120					125		

2

Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 5Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 10 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 15Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 20 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 25Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 30 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 35Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 40 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800



Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

5Ala

<210> 16

<211> 833

10<212> PRT

<213> Thermus scotoductus

<400> 16

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 15 1 5 10 15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45  
 20Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val  
 50 55 60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala  
 65 70 75 80  
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 25 85 90 95  
 Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu  
 100 105 110  
 Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
 115 120 125  
 30Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
 130 135 140  
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ser Ile Leu His Pro Glu Gly  
 145 150 155 160  
 Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro  
 35 165 170 175  
 Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn  
 180 185 190  
 Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile  
 195 200 205  
 40Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val  
 210 215 220

Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu  
 225 230 235 240  
 Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Glu Leu Pro Leu Gln  
 245 250 255  
 5Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 10 290 295 300  
 Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala  
 305 310 315 320  
 Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 15Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 20 370 375 380  
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 25Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Trp Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 30 450 455 460  
 Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 35Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 40 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 5Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 10625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 15Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 20705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 25Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 30785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 35Ala

&lt;210&gt; 17

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A *Thermus scotoductus* nucleic acid polymerase polypeptide from strain X-1 in which Asp is used in place of Gly at position 46.

10&lt;400&gt; 17

```

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1             5             10             15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
      20             25             30
15Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Asp Phe Ala
      35             40             45
Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val
      50             55             60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala
2065             70             75             80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
      85             90             95
Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu
      100            105            110
25Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
      115            120            125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
      130            135            140
Leu Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly
30145            150            155            160
Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro
      165            170            175
Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn
      180            185            190
35Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile
      195            200            205
Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val
      210            215            220
Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu
40225            230            235            240
Lys Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Gln
      245            250            255

```

Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala			
			260					265					270					
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu			
			275				280					285						
5Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu			
			290				295				300							
Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala			
305					310					315					320			
Glu	Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala			
10				325					330					335				
Glu	Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu			
			340					345					350					
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu			
			355				360					365						
15Ala	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser			
			370			375					380							
Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr			
385					390					395					400			
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala			
20				405					410				415					
Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu			
			420					425					430					
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr			
			435				440					445						
25Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val			
			450			455					460							
Glu	Ala	Glu	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly			
465					470					475					480			
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe			
30				485					490				495					
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys			
			500					505				510						
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro			
			515				520					525						
35Ile	Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly			
			530			535					540							
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg			
545					550					555					560			
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser			
40				565					570				575					
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly			
			580					585					590					

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 5Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 10 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 15Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 20 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 25His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 30 820 825 830  
 Ala

&lt;210&gt; 18

&lt;211&gt; 830

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A Thermus scotoductus nucleic acid polymerase polypeptide from strain X-1 in which Asp is used in place of Gly at position 46.

10&lt;400&gt; 18

Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
1				5				10						15	
His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		20						25					30		
15Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Asp	Phe	Ala	Lys	Ser	Leu
		35					40					45			
Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	Phe	Asp
	50					55					60				
Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	Lys	Ala
2065					70					75				80	
Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
				85					90					95	
Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	Pro	Gly
		100						105					110		
25Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	Glu	Lys
		115						120					125		
Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	Tyr	Gln
		130					135					140			
Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	Leu	Ile
30145					150					155				160	
Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	Gln	Trp
			165						170					175	
Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	Pro	Gly
			180					185					190		
35Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	Glu	Trp
		195					200					205			
Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	Pro	Ala
		210					215					220			
Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys	Leu	Ser
40225					230					235				240	
Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Gln	Val	Asp	Phe
				245					250					255	

Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu  
 260 265 270  
 Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser  
 275 280 285  
 5Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe  
 290 295 300  
 Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn  
 305 310 315 320  
 Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala Glu Asp Pro  
 10 325 330 335  
 Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu Ala Lys  
 340 345 350  
 Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala Pro Gly  
 355 360 365  
 15Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Ala  
 370 375 380  
 Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala  
 385 390 395 400  
 Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu Leu Glu  
 20 405 410 415  
 Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val Glu  
 420 425 430  
 Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg  
 435 440 445  
 25Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu Ala Glu  
 450 455 460  
 Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly His Pro Phe  
 465 470 475 480  
 Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 30 485 490 495  
 Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 500 505 510  
 Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Asp  
 515 520 525  
 35Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr Tyr Ile  
 530 535 540  
 Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu His Thr  
 545 550 555 560  
 Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 40 565 570 575  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 580 585 590



Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val Leu Asp  
           595                                600                                605  
 Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
           610                                615                                620  
 5Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr Gln Thr  
       625                                630                                635                                640  
 Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser Leu Met  
                                 645                                650                                655  
 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser  
 10                                660                                665                                670  
 Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val  
           675                                680                                685  
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala Trp  
           690                                695                                700  
 15Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val Glu Thr  
       705                                710                                715                                720  
 Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val Lys  
                                 725                                730                                735  
 Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
 20                                740                                745                                750  
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
           755                                760                                765  
 Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp Glu  
           770                                775                                780  
 25Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala Gln Glu  
       785                                790                                795                                800  
 Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro Leu Glu  
                                 805                                810                                815  
 Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
 30                                820                                825                                830

<210> 19

<211> 833

<212> PRT

35<213> Artificial Sequence

<220>

<223> A *Thermus scotoductus* nucleic acid polymerase polypeptide from strain SM3 in which Asp is used in place of Gly at position 46.

<400> 19

Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
5			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Asp	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
	50					55					60				
10Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
	65				70				75					80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
				85					90					95	
Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
15			100					105					110		
Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
			115				120						125		
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130					135					140				
20Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly
	145				150					155				160	
Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro
				165					170					175	
Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn
25			180					185					190		
Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile
			195				200					205			
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val
	210					215					220				
30Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu
	225				230					235				240	
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Glu	Leu	Pro	Leu	Gln
				245					250					255	
Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala
35			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
			275				280					285			
Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
40Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala
	305				310					315				320	

Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 5Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Gln Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 10385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 15Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Trp Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 20465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 25Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 30545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 35Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 40625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655

Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 5Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 10 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 15Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 20 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Ala

25

&lt;210&gt; 20

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

30

&lt;220&gt;

<223> A *Thermus scotoductus* nucleic acid polymerase polypeptide from  
 strain Vi7a in which Asp is used in place of Gly at position 46.

35&lt;400&gt; 20

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30  
 40Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Asp Phe Ala  
 35 40 45

Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val  
 50 55 60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala  
 65 70 75 80  
 5Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 85 90 95  
 Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu  
 100 105 110  
 Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
 10 115 120 125  
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
 130 135 140  
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ser Ile Leu His Pro Glu Gly  
 145 150 155 160  
 15Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro  
 165 170 175  
 Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn  
 180 185 190  
 Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile  
 20 195 200 205  
 Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val  
 210 215 220  
 Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu  
 225 230 235 240  
 25Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Glu Leu Pro Leu Gln  
 245 250 255  
 Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 30 275 280 285  
 Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala  
 305 310 315 320  
 35Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 40 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
385						390				395					400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	
				405					410					415		
5	Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu
				420					425					430		
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
				435				440				445				
Gly	Val	Trp	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	
10		450					455				460					
Glu	Ala	Glu	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	
				465			470			475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
				485					490					495		
15	Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys
				500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
				515				520				525				
Ile	Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	
20		530					535				540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	
				545			550			555					560	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
25	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
				580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	
				595				600				605				
Val	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
30		610					615				620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	
				625			630			635					640	
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	
				645					650					655		
35	Ser	Leu	Met	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
				660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
				675				680				685				
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	
40		690					695				700					
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Ala	Glu	Gly	Arg	Glu	Arg	Gly	Tyr	
				705			710			715					720	

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
                     725                    730                    735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                    745                    750  
 5Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                    760                    765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
                     770                    775                    780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 10785                    790                    795                    800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
                     805                    810                    815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                    825                    830  
 15Ala

<210> 21

<211> 833

20<212> PRT

<213> Artificial Sequence

<220>

<223> A derivative *Thermus scotoductus* polypeptide from strain X-1 in  
 25 which Tyr is used in place of Phe at position 668.

<400> 21

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
   1                    5                    10                    15  
 30Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
                     20                    25                    30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
                     35                    40                    45  
 Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val  
 35  50                    55                    60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala  
   65                    70                    75                    80  
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
                     85                    90                    95  
 40Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu  
                     100                    105                    110

Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	
		115					120				125					
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	
		130				135				140						
5Leu	Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	
		145			150				155						160	
Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	
			165					170						175		
Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	
10			180					185					190			
Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	
		195					200				205					
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	
		210				215					220					
15Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	
		225			230				235						240	
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Gln	
			245					250						255		
Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	
20			260					265					270			
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
		275					280					285				
Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	
		290				295					300					
25Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	
		305			310				315						320	
Glu	Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala	
			325					330					335			
Glu	Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu	
30			340					345					350			
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	
		355					360					365				
Ala	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
		370				375					380					
35Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
		385			390				395						400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	
			405					410					415			
Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	
40			420					425					430			
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				



Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 465 470 475 480  
 5His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 10 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 545 550 555 560  
 15Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 20 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 25Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 30 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 35Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 40 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

10

<211> 830

<223> A derivative *Thermus scotoductus* polypeptide from strain X-1 in which Tyr is used in place of Phe at position 668.

20	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
	1				5					10					15	
	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	Thr	Thr
				20					25					30		
	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
25			35					40					45			
	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	Phe	Asp
		50					55					60				
	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	Lys	Ala
	65					70					75					80
30	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
					85					90					95	
	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	Pro	Gly
				100					105						110	
	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	Glu	Lys
35			115					120					125			
	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	Tyr	Gln
		130					135					140				
	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	Leu	Ile
	145					150					155					160
40	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	Gln	Trp
				165						170					175	

Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly  
 180 185 190  
 Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg Glu Trp  
 195 200 205  
 5Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys Pro Ala  
 210 215 220  
 Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys Leu Ser  
 225 230 235 240  
 Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Gln Val Asp Phe  
 10 245 250 255  
 Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu  
 260 265 270  
 Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser  
 275 280 285  
 15Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe  
 290 295 300  
 Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn  
 305 310 315 320  
 Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala Glu Asp Pro  
 20 325 330 335  
 Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu Ala Lys  
 340 345 350  
 Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala Pro Gly  
 355 360 365  
 25Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Ala  
 370 375 380  
 Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala  
 385 390 395 400  
 Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu Leu Glu  
 30 405 410 415  
 Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val Glu  
 420 425 430  
 Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg  
 435 440 445  
 35Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu Ala Glu  
 450 455 460  
 Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly His Pro Phe  
 465 470 475 480  
 Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 40 485 490 495  
 Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 500 505 510

Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Asp  
 515 520 525  
 Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr Tyr Ile  
 530 535 540  
 5Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu His Thr  
 545 550 555 560  
 Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 565 570 575  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 10 580 585 590  
 Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val Leu Asp  
 595 600 605  
 Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
 610 615 620  
 15Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr Gln Thr  
 625 630 635 640  
 Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser Leu Met  
 645 650 655  
 Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr Gly Met Ser  
 20 660 665 670  
 Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val  
 675 680 685  
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala Trp  
 690 695 700  
 25Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val Glu Thr  
 705 710 715 720  
 Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val Lys  
 725 730 735  
 Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
 30 740 745 750  
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
 755 760 765  
 Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp Glu  
 770 775 780  
 35Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala Gln Glu  
 785 790 795 800  
 Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro Leu Glu  
 805 810 815  
 Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
 40 820 825 830

&lt;210&gt; 23

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

<223> A derivative *Thermus scotoductus* polypeptide from strain SM3 in which Tyr is used in place of Phe at position 668.

10&lt;400&gt; 23

Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
15Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
	50				55				60						
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
2065				70				75						80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
			85					90					95		
Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
			100					105					110		
25Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
			115					120					125		
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130						135					140			
Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly
30145				150					155					160	
Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro
			165					170					175		
Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn
			180					185					190		
35Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile
			195					200					205		
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val
	210				215						220				
Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu
40225				230					235					240	
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Glu	Leu	Pro	Leu	Gln
			245						250					255	

Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala		
260	265	270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu		
275	280	285
5Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu		
290	295	300
Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala		
305	310	315
Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala		
10 325	330	335
Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu		
340	345	350
Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu		
355	360	365
15Ala Gln Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser		
370	375	380
Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr		
385	390	395
Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala		
20 405	410	415
Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu		
420	425	430
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr		
435	440	445
25Gly Val Trp Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val		
450	455	460
Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly		
465	470	475
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe		
30 485	490	495
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys		
500	505	510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro		
515	520	525
35Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly		
530	535	540
Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg		
545	550	555
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser		
40 565	570	575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly		
580	585	590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 5Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr  
 10 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 15Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 20 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 25His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 30 820 825 830  
 Ala

<210> 24

35<211> 833

<212> PRT

<213> Artificial Sequence

<220>

40<223> A derivative *Thermus scotoductus* polypeptide from strain Vi7a in which Tyr is used in place of Phe at position 668.

<400> 24

Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
5			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
		35					40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
	50					55					60				
10Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
65					70				75					80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
				85					90					95	
Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
15			100					105					110		
Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
		115					120					125			
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130						135					140			
20Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly
145					150					155				160	
Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro
				165					170				175		
Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn
25			180					185					190		
Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile
		195					200					205			
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val
	210					215						220			
30Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu
225					230					235				240	
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Glu	Leu	Pro	Leu	Gln
			245						250				255		
Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala
35			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
40Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala
305					310					315				320	



Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 5Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 10385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 15Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Trp Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 20465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 25Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 30545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 35Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 40625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655

Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr  
                   660                  665                  670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
                   675                  680                  685  
 5Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
                   690                  695                  700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705                  710                  715                  720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 10                  725                  730                  735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                   740                  745                  750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                   755                  760                  765  
 15Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
                   770                  775                  780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785                  790                  795                  800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 20                  805                  810                  815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                   820                  825                  830  
 Ala

25

&lt;210&gt; 25

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

30

&lt;220&gt;

<223> A derivative *Thermus scotoductus* polypeptide from strain X-1 in  
 which Asp is used in place of Gly at position 46 and Tyr in place of  
 Phe at position 668.

35

&lt;400&gt; 25

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
   1                  5                  10                  15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 40                  20                  25                  30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Asp Phe Ala  
                   35                  40                  45

Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val  
 50 55 60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala  
 65 70 75 80  
 5Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 85 90 95  
 Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu  
 100 105 110  
 Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
 10 115 120 125  
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
 130 135 140  
 Leu Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly  
 145 150 155 160  
 15Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro  
 165 170 175  
 Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn  
 180 185 190  
 Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile  
 20 195 200 205  
 Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val  
 210 215 220  
 Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu  
 225 230 235 240  
 25Lys Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Gln  
 245 250 255  
 Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 30 275 280 285  
 Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala  
 305 310 315 320  
 35Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 40 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr															
385					390				395						400
Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala															
				405				410						415	
5Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu															
				420				425						430	
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr															
				435				440						445	
Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val															
10 450						455								460	
Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly															
465						470								475	480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe															
				485				490							495
15Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys															
				500				505						510	
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro															
				515				520						525	
Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly															
20 530						535								540	
Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg															
545						550								555	560
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser															
				565				570							575
25Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly															
				580				585						590	
Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val															
				595				600						605	
Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser															
30 610						615								620	
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His															
625						630								635	640
Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp															
				645				650							655
35Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr															
				660				665						670	
Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu															
				675				680						685	
Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val															
40 690						695								700	
Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr															
705						710								715	720

Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala	Ser
725					730					735					
Arg	Val	Lys	Ser	Ile	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
740					745					750					
5Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
755					760					765					
Leu	Phe	Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
770					775					780					
His	Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val
10785	790					795					800				
Ala	Gln	Glu	Ala	Lys	Arg	Thr	Met	Glu	Glu	Val	Trp	Pro	Leu	Lys	Val
805					810					815					
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
820					825					830					
15Ala															

<210> 26

<211> 830

20<212> PRT

<213> Artificial Sequence

<220>

25 <223> A derivative *Thermus scotoductus* polypeptide from strain X-1 in  
which Asp is used in place of Gly at position 46 and Tyr in place of  
Phe at position 668.

<400> 26

	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
30	1					5				10					15	
	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	Thr	Thr
				20					25					30		
	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Asp	Phe	Ala	Lys	Ser	Leu
			35					40					45			
35	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	Phe	Asp
	50						55					60				
	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	Lys	Ala
	65					70					75				80	
	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
40					85					90					95	
	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	Pro	Gly
				100					105					110		

Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	Glu	Lys			
		115					120					125						
Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	Tyr	Gln			
		130				135					140							
5Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	Leu	Ile			
		145			150				155						160			
Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	Gln	Trp			
			165					170						175				
Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	Pro	Gly			
10			180				185						190					
Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	Glu	Trp			
		195				200					205							
Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	Pro	Ala			
		210			215				220									
15Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys	Leu	Ser			
		225			230				235						240			
Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Gln	Val	Asp	Phe			
			245					250						255				
Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	Leu	Glu			
20			260					265					270					
Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	Ser			
		275				280					285							
Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe			
		290				295					300							
25Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Asn			
		305			310					315					320			
Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala	Glu	Asp	Pro			
			325					330					335					
Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys			
30			340				345					350						
Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	Ala	Pro	Gly			
		355				360					365							
Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Ala			
		370				375					380							
35Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	Ala			
		385			390					395					400			
Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	Leu	Leu	Glu			
			405					410					415					
Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val	Glu			
40			420					425					430					
Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg			
		435					440						445					

Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu Ala Glu  
 450 455 460  
 Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly His Pro Phe  
 465 470 475 480  
 5Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 485 490 495  
 Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 500 505 510  
 Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Asp  
 10 515 520 525  
 Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr Tyr Ile  
 530 535 540  
 Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu His Thr  
 545 550 555 560  
 15Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 565 570 575  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 580 585 590  
 Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val Leu Asp  
 20 595 600 605  
 Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
 610 615 620  
 Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr Gln Thr  
 625 630 635 640  
 25Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser Leu Met  
 645 650 655  
 Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr Gly Met Ser  
 660 665 670  
 Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val  
 30 675 680 685  
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala Trp  
 690 695 700  
 Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val Glu Thr  
 705 710 715 720  
 35Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val Lys  
 725 730 735  
 Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
 740 745 750  
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
 40 755 760 765  
 Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp Glu  
 770 775 780

Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala Gln Glu  
 785                                      790                                      795                                      800  
 Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro Leu Glu  
    805                                      810                                      815  
 5Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
    820                                      825                                      830

<210> 27

<211> 833

10<212> PRT

<213> Artificial Sequence

<220>

<223> A derivative *Thermus scotoductus* polypeptide from strain SM3 in  
 15        which Asp is used in place of Gly at position 46 and Tyr in place of  
           Phe at position 668.

<400> 27

Met Arg Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 20 1                                      5                                      10                                      15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
    20                                      25                                      30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Asp Phe Ala  
    35                                      40                                      45  
 25Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val  
    50                                      55                                      60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala  
 65                                      70                                      75                                      80  
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 30                                      85                                      90                                      95  
 Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu  
    100                                      105                                      110  
 Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
    115                                      120                                      125  
 35Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
    130                                      135                                      140  
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ser Ile Leu His Pro Glu Gly  
 145                                      150                                      155                                      160  
 Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro  
 40                                      165                                      170                                      175  
 Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn  
    180                                      185                                      190



Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile			
		195					200					205						
Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val			
		210				215				220								
5Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu			
		225			230					235				240				
Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Glu	Leu	Pro	Leu	Gln			
			245					250					255					
Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala			
10			260				265					270						
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu			
		275				280					285							
Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu			
		290			295					300								
15Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala			
		305			310				315				320					
Glu	Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala			
			325					330				335						
Glu	Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu			
20			340				345					350						
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu			
		355				360					365							
Ala	Gln	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser			
		370			375					380								
25Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr			
		385			390				395				400					
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala			
			405					410				415						
Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu			
30			420				425					430						
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr			
		435				440					445							
Gly	Val	Trp	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val			
		450			455					460								
35Glu	Ala	Glu	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly			
		465			470				475				480					
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe			
			485					490				495						
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys			
40			500				505					510						
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro			
			515				520					525						

Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 545 550 555 560  
 5Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 10 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 15Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 20 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 25Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 30 755 760 765  
 Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 35Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Ala

<213> Artificial Sequence

<220>

<223> A derivative *Thermus scotoductus* polypeptide from strain Vi7a in which Asp is used in place of Gly at position 46 and Tyr in place of Phe at position 668.

<400> 28

	Met	Arg	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
	1				5					10					15	
	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
15				20					25					30		
	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Asp	Phe	Ala
			35					40					45			
	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val
	50						55					60				
20	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala
65						70					75					80
	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
					85					90					95	
	Ala	Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu
25				100					105					110		
	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
			115					120					125			
	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130						135					140				
30	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly
145						150					155					160
	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro
					165					170					175	
	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn
35				180					185					190		
	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile
			195					200					205			
	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val
	210						215					220				
40	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu
225						230						235				240

Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Glu Leu Pro Leu Gln  
 245 250 255  
 Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala  
 260 265 270  
 5Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala  
 10305 310 315 320  
 Glu Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 15Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 20385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 25Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Trp Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly  
 30465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 35Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 40545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 5Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 10 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 15Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
 20 725 730 735  
 Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 25Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
 785 790 795 800  
 Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
 30 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Ala

35

&lt;210&gt; 29

&lt;211&gt; 18

&lt;212&gt; DNA

<213> *Thermus scotoductus*

40

&lt;400&gt; 29

ggccaccacc tggcctac

<210> 30  
 <211> 17  
 <212> DNA  
 <213> Thermus scotoductus  
 5  
 <400> 30  
 cccacctcca cctccag 17

<210> 31  
 10<211> 21  
 <212> DNA  
 <213> Thermus scotoductus

<400> 31  
 15ctggccatgc tgaagctctt t 21

<210> 32  
 <211> 27  
 <212> DNA  
 20<213> Thermus scotoductus

<400> 32  
 ataagggcga tgctgccct ctttgag 27

25<210> 33  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

30<220>  
 <223> 5' forward primer for the amplification of the full-length Thermus  
 scotoductus nucleic acid polymerase coding region.

<400> 33  
 35catatgaggg cgatgctgcc cctc 24

<210> 34  
 <211> 6  
 <212> DNA  
 <213> Artificial Sequence  
 5  
 <220>  
 <223> Recognition site for the restriction enzyme Nde I.  
  
 <400> 34  
 10catatg 6  
  
 <210> 35  
 <211> 18  
 <212> DNA  
 15<213> Thermus scotoductus  
  
 <400> 35  
 ctccacctcc aggggcac 18  
  
 20<210> 36  
 <211> 21  
 <212> DNA  
 <213> Thermus scotoductus  
  
 25<400> 36  
 ctggccatgg tgaagctctt t 21  
  
 <210> 37  
 <211> 6  
 30<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Recognition site for the restriction enzyme Sal I.  
 35  
 <400> 37  
 gtcgac 6  
  
 40

&lt;210&gt; 38

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

5

&lt;220&gt;

&lt;223&gt; A primer.

&lt;400&gt; 38

10gtcgactagg ccttggcgaa agcca

25

&lt;210&gt; 39

&lt;211&gt; 29

&lt;212&gt; PRT

15&lt;213&gt; Thermus scotoductus

&lt;400&gt; 39

Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val Phe

1

5

10

15

20Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu

20

25

&lt;210&gt; 40

&lt;211&gt; 36

25&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

&lt;400&gt; 40

Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu

30 1

5

10

15

Asn Leu Leu Lys His Leu Glu Gln Val Lys Pro Ala Ser Val Arg Glu

20

25

30

Lys Ile Leu Ser

35

35

40



&lt;210&gt; 41

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

5

&lt;400&gt; 41

Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn

1

5

10

15

Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala Glu Asp Pro

10

20

25

30

Leu Glu Ala Leu Arg Gly Leu Gly

35

40

&lt;210&gt; 42

15&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

&lt;400&gt; 42

20Arg Leu Tyr Ala Ala Leu Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu

1

5

10

15

Leu Trp Leu Tyr Glu

20

25&lt;210&gt; 43

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

30&lt;400&gt; 43

Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys

1

5

10

15

Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn

20

25

30

35

40

&lt;210&gt; 44

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

5

&lt;400&gt; 44

Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro  
 1 5 10 15  
 Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu  
 10 20 25 30  
 Ser Ala Lys Ala  
 35

&lt;210&gt; 45

15&lt;211&gt; 544

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

&lt;400&gt; 45

20Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 1 5 10 15  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 20 25 30  
 Leu Asn Ala Leu Ala Ala Ala Trp Glu Gly Arg Val Tyr Arg Ala Glu  
 25 35 40 45  
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 50 55 60  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 65 70 75 80  
 30Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 85 90 95  
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 100 105 110  
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 35 115 120 125  
 Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 130 135 140  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 145 150 155 160  
 40Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 165 170 175

Ala Glu Leu Arg Arg Leu Glu Glu Glu Val His Arg Leu Ala Gly His  
 180 185 190  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 195 200 205  
 5Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 210 215 220  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 225 230 235 240  
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 10 245 250 255  
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
 260 265 270  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 275 280 285  
 15Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 290 295 300  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
 305 310 315 320  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 20 325 330 335  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
 340 345 350  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
 355 360 365  
 25Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 370 375 380  
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
 385 390 395 400  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
 30 405 410 415  
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
 420 425 430  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
 435 440 445  
 35Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 450 455 460  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 465 470 475 480  
 Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His  
 40 485 490 495  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala  
 500 505 510

10

•

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr		
	245	250 255
Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu		
	260	265 270
5His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser		
	275	280 285
Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln		
	290	295 300
Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val		
10305	310	315 320
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly		
	325	330 335
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr		
	340	345 350
15Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser		
	355	360 365
Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly		
	370	375 380
Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu		
20385	390	395 400
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg		
	405	410 415
Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val		
	420	425 430
25Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg		
	435	440 445
Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro		
	450	455 460
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu		
30465	470	475 480
Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His		
	485	490 495
Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala		
	500	505 510
35Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro		
	515	520 525
Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala		
	530	535 540

&lt;210&gt; 47

&lt;211&gt; 544

&lt;212&gt; PRT

&lt;213&gt; Thermus scotoductus

5

&lt;400&gt; 47

Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
1				5					10					15	
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu
10			20					25					30		
Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala	Glu
			35				40					45			
Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu	Leu
			50			55				60					
15Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	Ala
65					70					75				80	
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn
					85				90					95	
Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu
20			100					105					110		
Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	Leu
			115					120				125			
Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu
			130					135				140			
25Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly
145					150					155				160	
Val	Trp	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	Glu
					165					170				175	
Ala	Glu	Leu	Arg	Arg	Leu	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	His
30			180					185					190		
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp
			195				200					205			
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg
			210				215					220			
35Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile
225					230					235				240	
Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	Thr
					245					250				255	
Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	Leu
40			260					265					270		
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
			275					280					285		

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 290 295 300  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
 305 310 315 320  
 5Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 325 330 335  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
 340 345 350  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
 10 355 360 365  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 370 375 380  
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
 385 390 395 400  
 15Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
 405 410 415  
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
 420 425 430  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
 20 435 440 445  
 Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 450 455 460  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 465 470 475 480  
 25Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His  
 485 490 495  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala  
 500 505 510  
 Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro  
 30 515 520 525  
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
 530 535 540

<210> 48

35<211> 832

<212> PRT

<213> Thermus aquaticus

<400> 48

40Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45  
 5Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val  
 50 55 60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly  
 65 70 75 80  
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 10 85 90 95  
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu  
 100 105 110  
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys  
 115 120 125  
 15Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp  
 130 135 140  
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly  
 145 150 155 160  
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
 20 165 170 175  
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
 180 185 190  
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
 195 200 205  
 25Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
 210 215 220  
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
 225 230 235 240  
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
 30 245 250 255  
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 35Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
 40 325 330 335  
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
 340 345 350



Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 5Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
 405 410 415  
 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
 10 420 425 430  
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 15Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 20 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 530 535 540  
 25Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 30 580 585 590  
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 35Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 40 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685

Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
690						695				700					
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val
705					710					715					720
5Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740						745					750	
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
10		755					760					765			
Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
		770				775					780				
Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790					795					800
15Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu
			820					825						830	

20&lt;210&gt; 49

&lt;211&gt; 834

&lt;212&gt; PRT

&lt;213&gt; Thermus thermophilus

25&lt;400&gt; 49

Met	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
30Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
		35					40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
		50				55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
3565					70					75				80	
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
40Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
			115					120					125		

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
 130 135 140  
 Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
 145 150 155 160  
 5Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
 10 195 200 205  
 Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
 225 230 235 240  
 15Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 20 275 280 285  
 Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 25Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 30 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 35Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 40 435 440 445  
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460

	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	
	465					470					475					480	
	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	
					485					490					495		
5	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	
				500					505					510			
	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	
			515					520						525			
	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	
10		530					535						540				
	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	
	545					550					555					560	
	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	
					565					570					575		
15	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	
				580					585					590			
	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	
			595				600						605				
	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	
20		610					615						620				
	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	
	625					630					635					640	
	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	
					645					650					655		
25	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	
				660					665					670			
	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	
			675					680					685				
	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	
30		690					695						700				
	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	
	705					710					715					720	
	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	
					725					730					735		
35	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	
				740					745					750			
	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	
			755					760					765				
	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	
40		770					775						780				
	Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	
	785					790					795				800		

10

10<212> PRT

4

2

Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp Leu His			
225	230	235	240
Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu Glu Val			
	245	250	255
5Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly Leu Arg			
	260	265	270
Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly			
	275	280	285
Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro			
10 290	295	300	
Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro Met Trp			
305	310	315	320
Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Glu Gly Arg Val His Arg			
	325	330	335
15Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly			
	340	345	350
Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala			
	355	360	365
Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro			
20 370	375	380	
Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe			
385	390	395	400
Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln			
	405	410	415
25Asn Leu Phe Pro Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu			
	420	425	430
Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly			
	435	440	445
Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu			
30 450	455	460	
Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His			
465	470	475	480
Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp			
	485	490	495
35Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Glu Lys Thr Gly Lys Arg			
	500	505	510
Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile			
	515	520	525
Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr			
40 530	535	540	
Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu			
545	550	555	560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 5Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala  
 595 600 605  
 Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr  
 10625 630 635 640  
 Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro  
 645 650 655  
 Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 15Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu  
 675 680 685  
 Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val  
 20705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
 725 730 735  
 Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 25Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys  
 30785 790 795 800  
 Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln  
 820 825 830  
 35Asp